Supporting Information for

A Monofunctional Platinum Complex Coordinated to a Rhodium Metalloinsertor Selectively Binds Mismatched DNA in the Minor Groove

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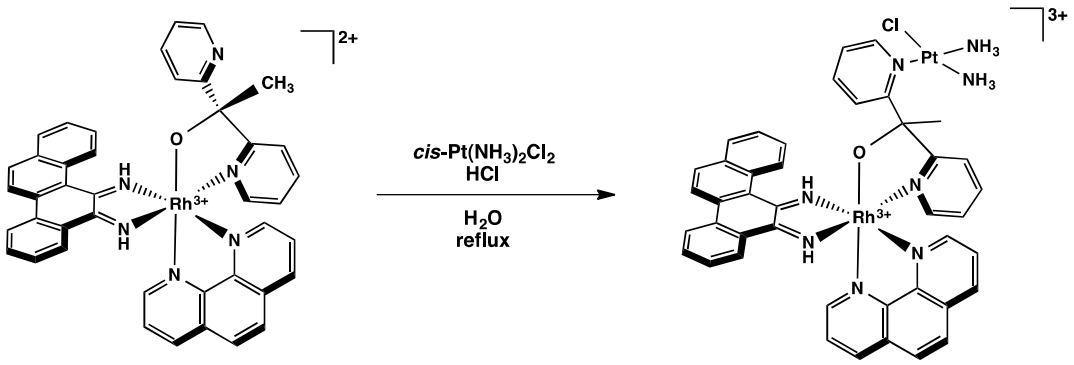


Scheme S1. Synthesis of $[Rh(chrysi)(phen)(DPE\text{-}Pt(NH_3)_2Cl]^{3+}$

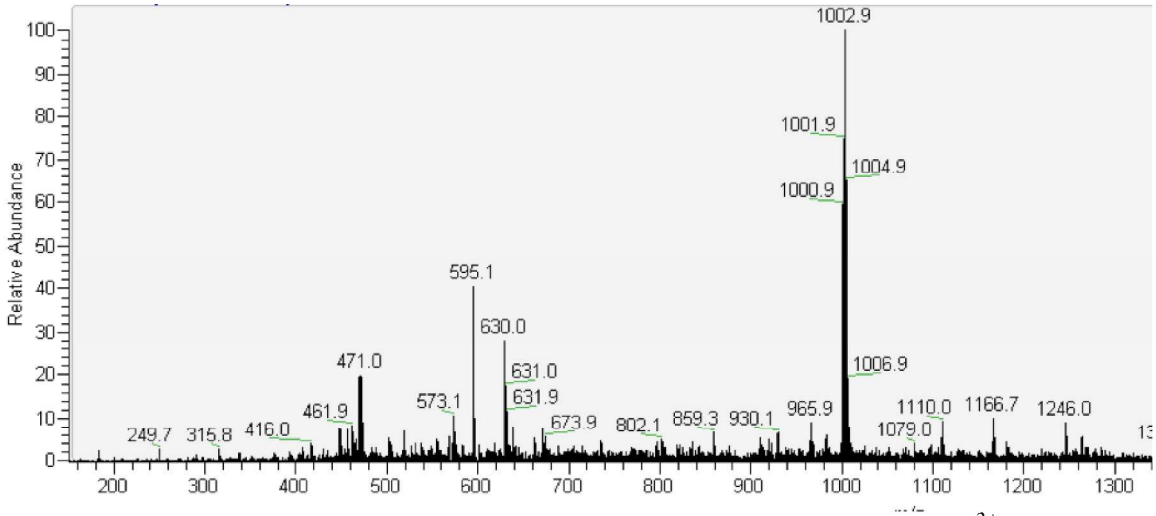


Figure S1. ESI-MS spectrum of $[Rh(chrysi)(phen)(DPE\text{-}Pt(NH_3)_2Cl]^{3+}$; *m/z* = 1000.9 – 1006.9 (indicative of the Rh and Pt isotope patterns), calc 1003.251.

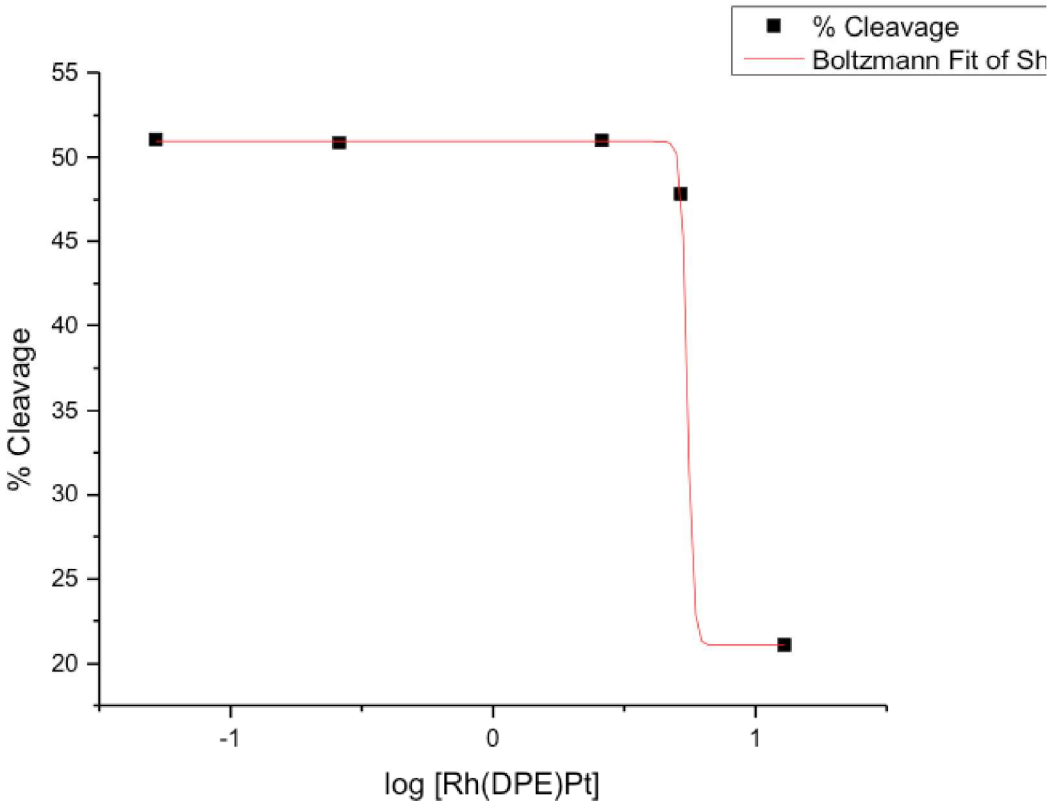


Figure S2. Representative sigmoidal curve (Boltzmann fit) of photocleavage competition titrations of [Rh(chrysi)(phen)(DPE-Pt(NH_3)$_2$Cl)]$^{3+}$ for binding constant determination at the CC mismatch. K_B was calculated by solving simultaneous equilibria at the inflection point of the curve. Experiments were conducted in buffer (50 mM NaCl, 10 mM NaP_i, pH 7.1) using 1 μM hairpin DNA and 1 μM rac-[Rh(bpy)$_2$chrysi]$^{3+,}$ with 0-15 μM [Rh(chrysi)(phen)(DPE-Pt(NH_3)$_2$Cl)]$^{3+}$competitor complex. Experiments were carried under conditions minimizing Pt coordination.

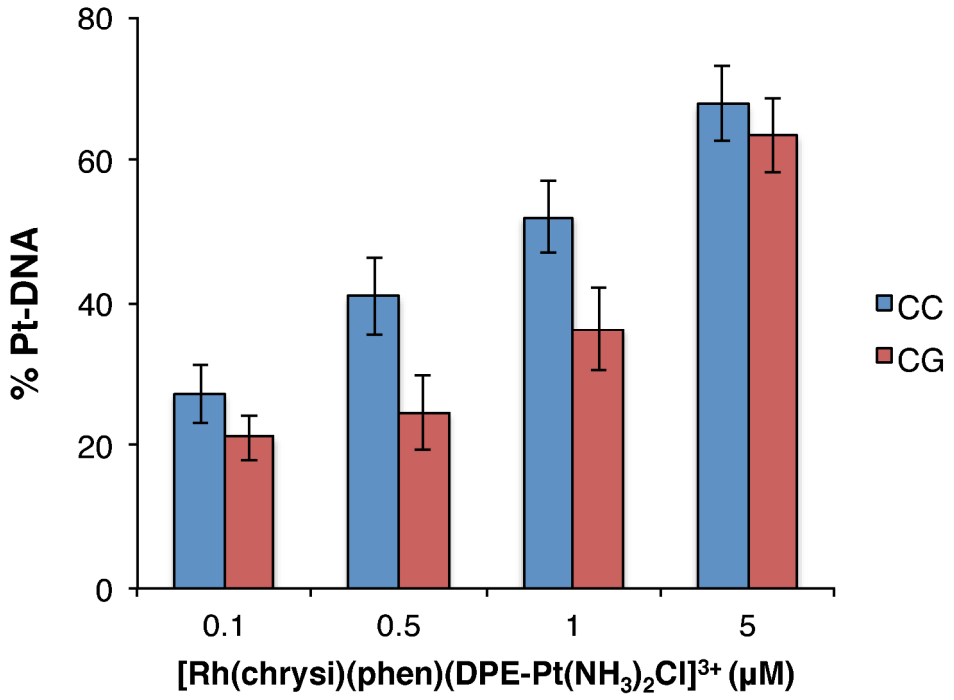
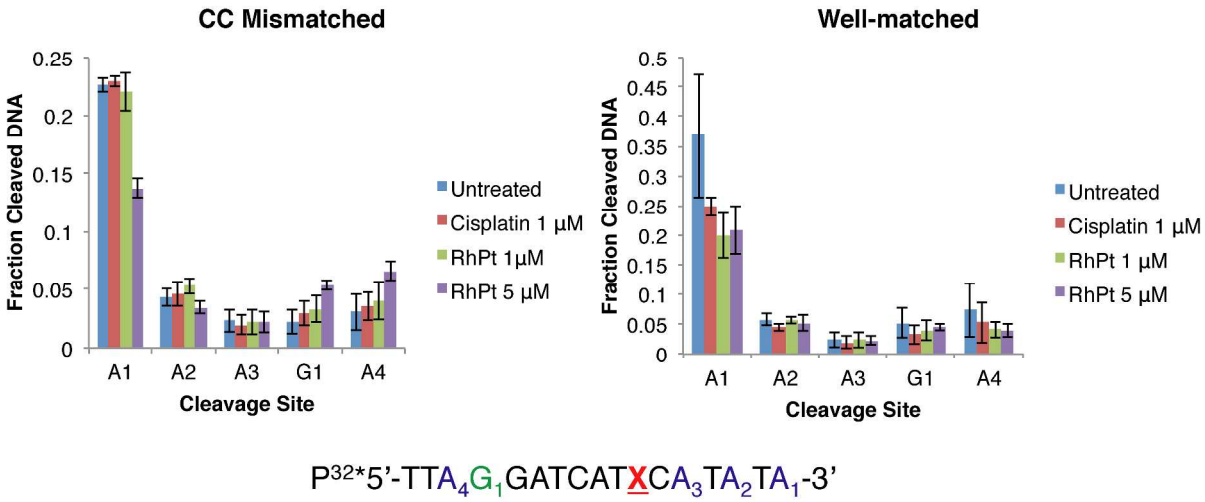


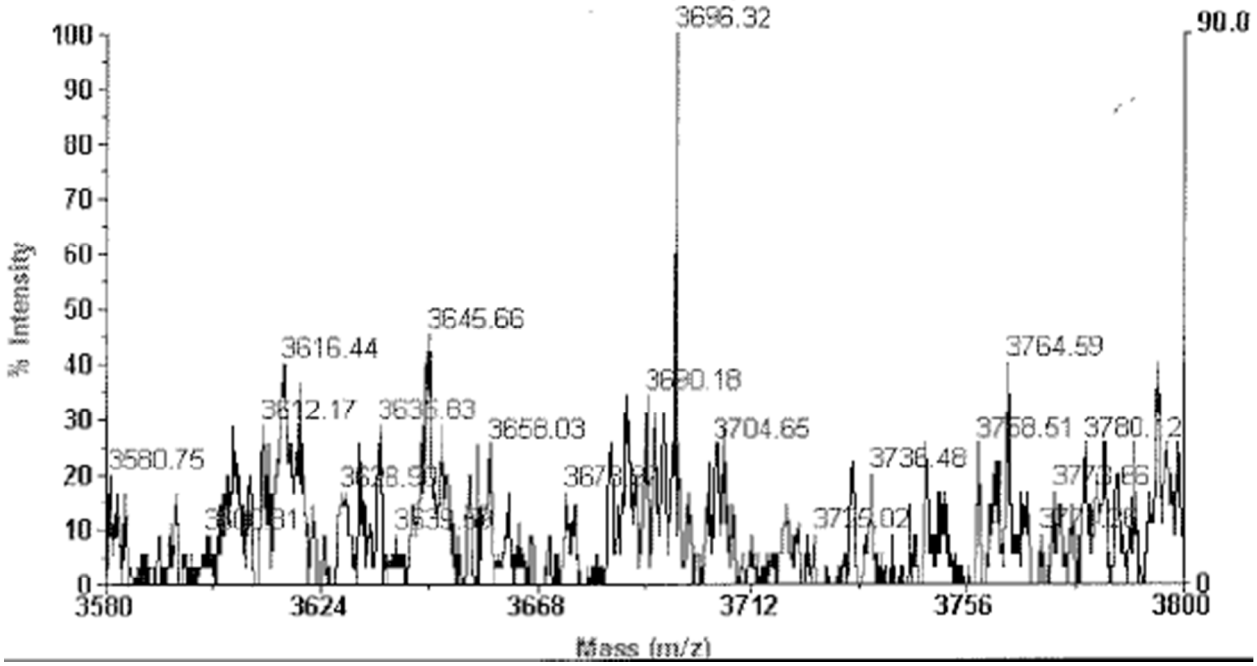
Figure S3. Quantification of platination of mismatched (CC, blue) and well-matched (CG, red) duplex DNA (1 μM) by $[Rh(chrysi)(phen)(DPE\text{-}Pt(NH_3)_2Cl)]^{3+}$ (0.1 – 5 μM). Samples were incubated at 37 °C for 2h and electrophoresed on a 20% denaturing PAGE gel. The amount of platinated DNA (% Pt-DNA) is expressed as a fraction of the total DNA in each sample.

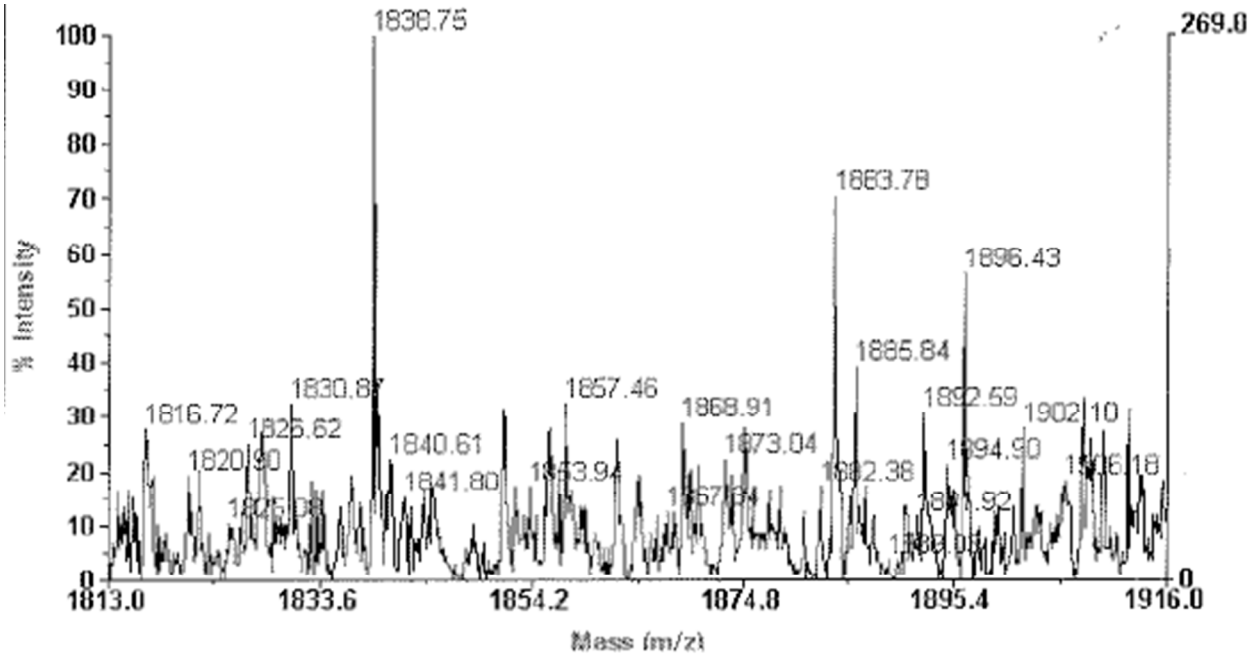


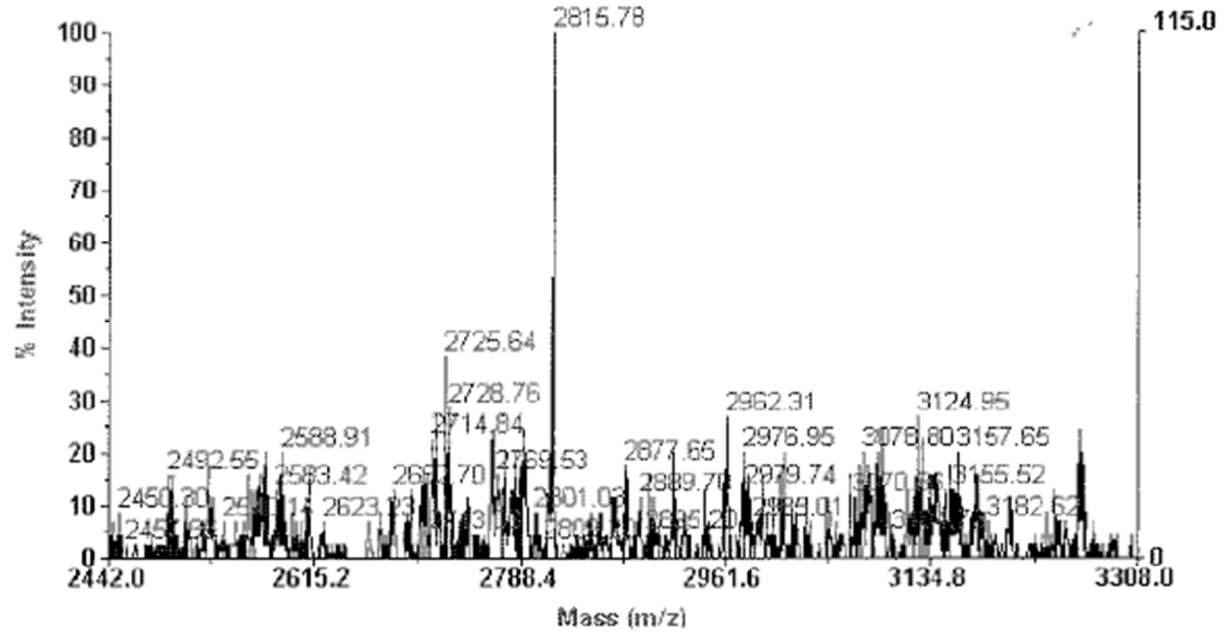
P^{32}*5'-TT$A_4$$G_1$GATCATXC$A_3TA_2TA_1$-3'

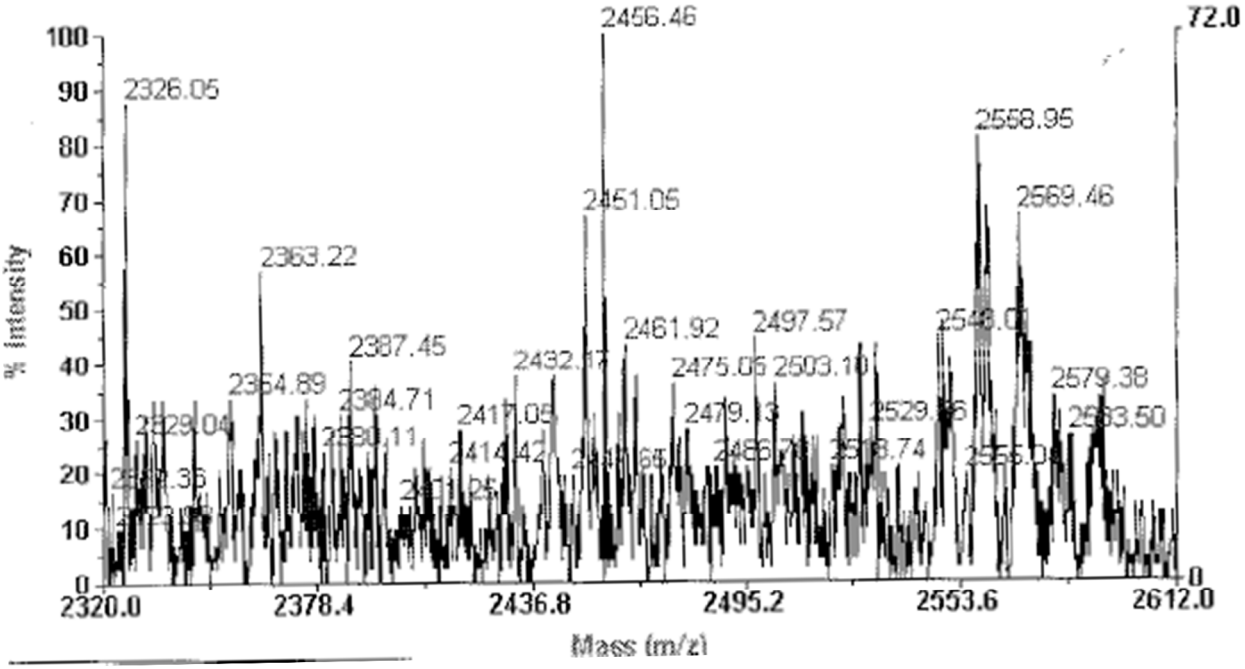
Figure S4. Quantification of DNA footprinting by methyl methanesulfonate (MMS) at purine residues (*N*3-adenine and *N*7-guanine) in mismatched (left) and well-matched (right) radiolabeled DNA of the sequence indicated. The site of the CC mismatch is denoted by the red 'X.' The location of each site of cleavage (A1, A2, A3, A4 = *N*3-adenine methylation, denoted in the sequence in blue; G1 = *N*7-guanine methylation, denoted in green) is indicated in the sequence. Not all purines in the labeled strand were susceptible to MMS-induced depurination. Duplex DNA was platinated with cisplatin (1 μM, red bars), the metalloinsertor conjugate (1 or 5 μM; green and purple bars, respectively), or left untreated (blue bars), alkylated with MMS, and depurinated at methylated sites. The cleaved DNA was electrophoresed on a 20% denaturing PAGE gel, and the fraction of cleaved DNA at each site is expressed as a fraction of the total DNA in each sample.

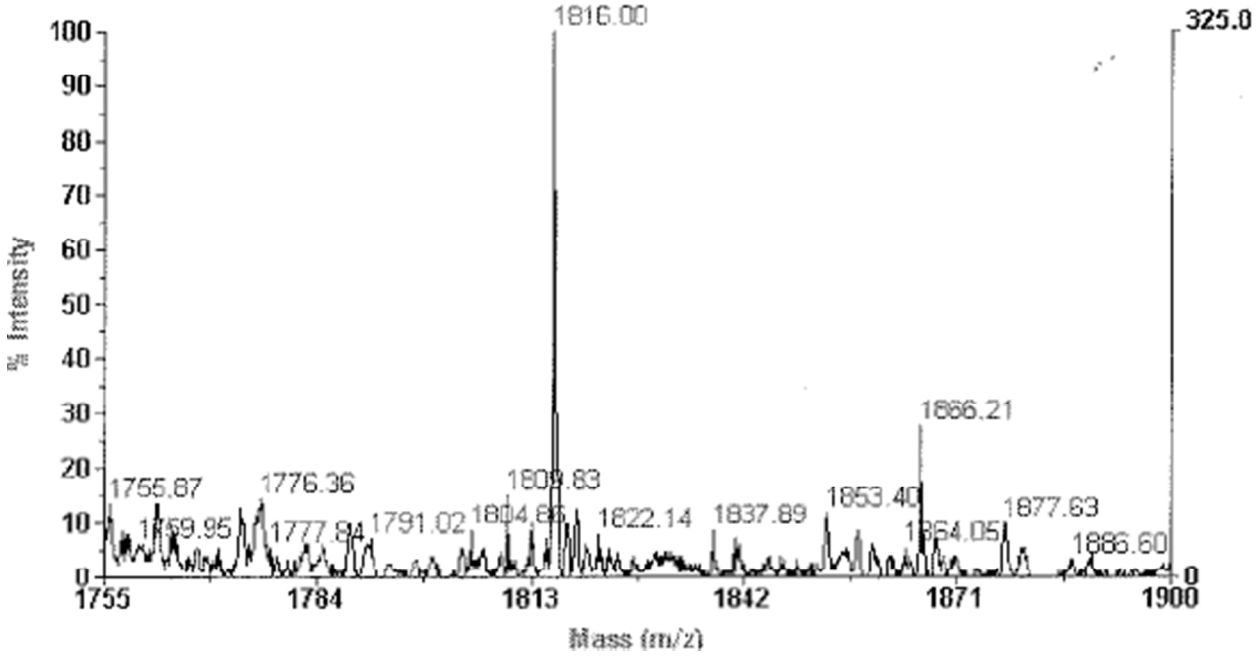
MALDI-TOF Mass Spectrometry of Platinated DNA Fragments






2815.78
115.0
100
90
80
70
60
50
40
30
20
10
0
% Intensity
2725.64
2728.76
2962.31
3124.95
2588.91
2976.95
2877.65
2492.55
2583.42
2450.30
2623.23
2889.70
2979.74
3155.52
3182.62
2442.0
2615.2
2788.4
2961.6
3134.8
3308.0
Mass (m/z)


2456.46
72.0
2326.05
2558.95
2569.46
2451.05
2363.22
2461.92
2497.57
2387.45
2475.06
2503.10
2579.38
2364.89
2479.13
2583.50
2529.36
2432.17
2417.08
2414.42
2486.78
2555.08
100
90
80
70
60
50
40
30
20
10
0
% Intensity
2320.0
2378.4
2436.8
2495.2
2553.6
2612.0
Mass (m/z)


1816.00
325.0
100
90
80
70
60
50
40
30
20
10
0
% Intensity
1886.21
1755.87
1776.36
1809.83
1853.40
1877.63
1759.95
1777.84
1791.02
1804.86
1822.14
1837.89
1864.05
1886.60
0
1755
1784
1813
1842
1871
1900
Mass (m/z)